

WEST Search History

DATE: Thursday, August 21, 2003

<u>Set Name</u>	<u>Query</u>	<u>Hit Count</u>	<u>Set Name</u>
side by side			result set
	DB=USPT; PLUR=YES; OP=AND		
L1	dam.clm.	3181	L1
L2	(\$methylase or methyltransferase\$ or methyl-transferase\$).clm.	241	L2
L3	L2 or dna.clm.	17060	L3
L4	L3 and l1	18	L4
L5	dam same (bacter\$ or microorgan\$ or salmonel\$ or shigel\$ or coli)	446	L5
L6	dam same (prokaryot\$ or procaryot\$)	13	L6
L7	L5 not l6 not l4	425	L7
L8	(\$methylase or methyltransferase\$ or methyl-transferase\$)	2250	L8
L9	L8 and l7	153	L9
L10	L9 and (heterologous or foreign or nonnative or recombinant or artificial or fusion)	152	L10
L11	L9 and (heterologous or foreign or nonnative or fusion)	121	L11
L12	L9 and (heterologous or foreign or nonnative or fusion)	121	L12
L13	(\$methylase or methyltransferase\$ or methyl-transferase\$ or dam) near50 (mutant or mutation or mutagenesis or alter\$ or mutants or mutations or insertion or deletion or modification or modified or truncated or truncation)	1690	L13

Search History Transcript

L14 L13 and l5

106 L14

DB=USPT,PGPB,JPAB,EPAB,DWPI,TDBD; PLUR=YES;

OP=AND

L15 dam.ti.

7503 L15

L16 L15 and dna

4 L16

END OF SEARCH HISTORY

05249481 86250633 PMID: 3522556

Mutant of *Salmonella typhimurium* LT2 deficient in DNA adenine methylation.

Ritchie L J; Hall R M; Podger D M

Journal of bacteriology (UNITED STATES) Jul 1986, 167 (1) p420-2,

ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

A mutant of *Salmonella typhimurium* LT2 deficient in methylation of the adenine residues in the sequence 5'- GATC -3' was isolated. The mutation (dam-1) was linked to the cysG locus, and the properties of the mutant were similar to those of *Escherichia coli* dam mutants. Reversion of the hisC3076 frameshift marker by 9-aminoacridine was substantially enhanced by the dam-1 mutation, implying a direct role for adenine methylation in the prevention of frameshift mutation induction.

Descriptors: Adenine--metabolism--ME; *DNA, Bacterial--metabolism--ME; *Mutation ; **Salmonella typhimurium*--genetics--GE; Aminacrine--pharmacology --PD; Genes, Bacterial; Methylation; Methyltransferases--genetics--GE; Methyltransferases--metabolism--ME; *Salmonella typhimurium*--metabolism--ME ; Site-Specific DNA-Methyltransferase (Adenine-Specific)

CAS Registry No.: 0 (DNA, Bacterial); 73-24-5 (Adenine); 90-45-9 (Aminacrine)

Enzyme No.: EC 2.1.1. (Methyltransferases); EC 2.1.1.72 (Site-Specific DNA-Methyltransferase (Adenine-Specific))

Record Date Created: 19860811

Record Date Completed: 19860811

10368256 96173077 PMID: 8589735

Adenine methylation at dam sites increases transient gene expression in plant cells.

Graham M W; Larkin P J
CSIRO Division of Plant Industry, Canberra, Australia.
Transgenic research (ENGLAND) Sep 1995, 4 (5) p324-31, ISSN
0962-8819 Journal Code: 9209120

Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

Escherichia coli encodes two major DNA methylation systems: dam, which produces 6-methyladenine; and dcm, which produces 5-methylcytosine. About 1-2% of adenine and cytosine residues in plasmid DNAs prepared in E. coli are methylated by these systems. Since DNA methylation profoundly influences gene expression in eukaryotes, we were interested in determining whether these bacterially encoded modifications might also effect plant gene expression in experimental systems. We therefore examined the influence of dam and dcm methylation on gene expression from four GUS fusion constructs in transient assays in protoplasts and microprojectile-bombarded whole tissues. In these constructs, GUS expression was driven by promoter regions derived from the Arabidopsis alcohol dehydrogenase (Adh1), maize ubiquitin (Ubi1), rice actin (Act1) and CaMV 35S genes. We show that methyladenine produced by dam methylation increased gene expression from constructs based on the Adh1, Ubi1 and Act1 genes. The increase in gene expression ranged from three-fold for Ubi1 and Adh1 in protoplasts to 50-fold for Act1 in bombarded wheat tissues. Expression of a 35S.GUS construct was, however, insensitive to dam methylation. dcm methylation had little if any effect on transient gene expression for any of these constructs. We provide indirect evidence that the critical sites of adenine methylation lie within sequences from the promoter regions, suggesting that dam methylation increases transcription rate. These results have important experimental implications and also raise the intriguing possibility that methyladenine might play a role in the regulation of gene expression in vivo.

Descriptors: Adenine --metabolism--ME; *Gene Expression Regulation, Plant; *Plants--genetics--GE; *Plants--metabolism--ME; Binding Sites; DNA Modification Methylases--metabolism--ME; Escherichia coli--metabolism--ME; Methylation; Plants--cytology--CY; Plants, Genetically Modified; Promoter Regions (Genetics); Recombinant Fusion Proteins--chemistry--CH; Recombinant Fusion Proteins--genetics--GE

CAS Registry No.: 0 (Recombinant Fusion Proteins); 73-24-5 (Adenine)

Enzyme No.: EC 2.1.1.- (DNA Modification Methylases)

Gene Symbol: Act1; Adh1; GUS; Ubi1

Record Date Created: 19960327

Record Date Completed: 19960327

06954574 91195052 PMID: 2014170

Molecular cloning and characterization of the gene encoding the adenine methyltransferase M.CviRI from Chlorella virus XZ-6E.

Stefan C; Xia Y N; Van Etten J L

Department of Plant Pathology, University of Nebraska, Lincoln
68583-0722.

Nucleic acids research (ENGLAND) Jan 25 1991, 19 (2) p307-11, ISSN
0305-1048 Journal Code: 0411011

Contract/Grant No.: GM-32441; GM; NIGMS

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The gene encoding the DNA methyltransferase M.CviRI from Chlorella virus XZ-6E was cloned and expressed in Escherichia coli. M.CviRI methylates adenine in TGCA sequences. DNA containing the M.CviRI gene was sequenced and a single open reading frame of 1137 bp was identified which could code for a polypeptide of 379 amino acids with a predicted molecular weight of 42,814. Comparison of the M.CviRI predicted amino acid sequence with another Chlorella virus and 14 bacterial adenine methyltransferases revealed extensive similarity to the other Chlorella virus enzyme.

Tags: Support, U.S. Gov't, Non-P.H.S.; Support, U.S. Gov't, P.H.S.

Descriptors: Chlorella; *DNA Modification Methylases--genetics--GE;
*Site-Specific DNA-Methyltransferase (Adenine -Specific)--genetics--GE;
*Viruses--enzymology--EN; Amino Acid Sequence; Base Sequence; Cloning,
Molecular; Escherichia coli--genetics--GE; Gene Expression Regulation,
Bacterial; Gene Expression Regulation, Enzymologic; Genes, Bacterial;
Molecular Sequence Data; Nucleic Acid Hybridization; Plasmids; Sequence
Alignment

Molecular Sequence Databank No.: GENBANK/M38173; GENBANK/X56859;
GENBANK/X56860; GENBANK/X56861; GENBANK/X56862; GENBANK/X56863;
GENBANK/X56864; GENBANK/X56865; GENBANK/X57509; GENBANK/X57510

CAS Registry No.: 0 (Plasmids)

Enzyme No.: EC 2.1.1.- (DNA Modification Methylases); EC 2.1.1.- (DNA
modification methylase CviRI); EC 2.1.1.72 (Site-Specific
DNA-Methyltransferase (Adenine -Specific))

Gene Symbol: M.CviRI

Record Date Created: 19910513

Record Date Completed: 19910513

06883099 91123209 PMID: 1846861

Two-step cloning and expression in *Escherichia coli* of the DNA restriction-modification system StyLTI of *Salmonella typhimurium*.

De Backer O; Colson C

Departement de Biologie, Universite Catholique de Louvain, Louvain-la-Neuve, Belgium.

Journal of bacteriology (UNITED STATES) Feb 1991, 173 (3) p1321-7,
ISSN 0021-9193 Journal Code: 2985120R

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The StyLTI restriction-modification system is common to most strains of the genus *Salmonella*, including *Salmonella typhimurium*. We report here the two-step cloning of the genes controlling the StyLTI system. The StyLTI methylase gene (*mod*) was cloned first. Then, the companion endonuclease gene (*res*) was introduced on a compatible vector. A strain of *S. typhimurium* sensitive to the coliphage lambda was constructed and used to select self-modifying recombinant phages from a Res- Mod+ *S. typhimurium* genomic library in the lambda EMBL4 cloning vector. The methylase gene of one of these phages was then subcloned in pBR328 and transferred into *Escherichia coli*. In the second step, the closely linked endonuclease and methylase genes were cloned together on a single DNA fragment inserted in pACYC184 and introduced into the Mod+ *E. coli* strain obtained in the first step. Attempts to transform Mod- *E. coli* or *S. typhimurium* strains with this Res+ Mod+ plasmid were unsuccessful, whereas transformation of Mod+ strains occurred at a normal frequency. This can be understood if the introduction of the StyLTI genes into naive hosts is lethal because of degradation of host DNA by restriction activity; in contrast to most restriction-modification systems, StyLTI could not be transferred into naive hosts without killing them. In addition, it was found that strains containing only the *res* gene are viable and lack restriction activity in the absence of the companion *mod* gene. This suggests that expression of the StyLTI endonuclease activity requires at least one polypeptide involved in the methylation activity, as is the case for types I and III restriction-modification systems but not for type II systems.

Tags: Support, Non-U.S. Gov't

Descriptors: DNA Modification Methylases--genetics--GE; *DNA Restriction Enzymes--genetics--GE; *Deoxyribonucleases, Type III Site-Specific --genetics--GE; **Escherichia coli*--genetics--GE; *Gene Expression Regulation, Bacterial; **Salmonella typhimurium*--genetics--GE; *Site-Specific DNA-Methyltransferase (Adenine -Specific)--genetics--GE; Cloning, Molecular; DNA Modification Methylases--metabolism--ME; DNA Restriction Enzymes--metabolism--ME; Deoxyribonucleases, Type III Site-Specific--metabolism--ME; Genes, Bacterial; Phenotype; Plasmids; Restriction Mapping; *Salmonella typhimurium*--enzymology--EN; Site-Specific DNA-Methyltransferase (Adenine -Specific)--metabolism--ME; Transformation, Bacterial

CAS Registry No.: 0 (Plasmids)

Enzyme No.: EC 2.1.1.- (DNA Modification Methylases); EC 2.1.1.- (DNA modification methylase StyLTI); EC 2.1.1.72 (Site-Specific DNA-Methyltransferase (Adenine -Specific)); EC 3.1.21 (DNA Restriction Enzymes); EC 3.1.21.- (endodeoxyribonuclease StyLTI); EC 3.1.21.5 (Deoxyribonucleases, Type III Site-Specific)

Gene Symbol: mod; res

Record Date Created: 19910311

Record Date Completed: 19910311

06560016 90185237 PMID: 2155857

DNA methylation in *Neisseria gonorrhoeae* and other *Neisseriae*.

Ritchot N; Roy P H

Departement de Biochimie, Faculte des Sciences et de Genie, Universite Laval, Sainte-Foy, Canada.

Gene (NETHERLANDS) Jan 31 1990, 86 (1) p103-6, ISSN 0378-1119

Journal Code: 7706761

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

It has been reported in the literature that *Neisseria gonorrhoeae* DNA is modified by the methyltransferases (MTases) M.NgoI, M.NgoII, and M.NgoIII, as well as three other cytosine MTases and one adenine MTase, even if the corresponding restriction endonucleases are not present. We envisioned the possibility of cloning one of the *N. gonorrhoeae* MTase-encoding genes for use as a species-specific DNA probe. We therefore undertook a survey of methylation patterns of several clinical isolates of *N. gonorrhoeae* and *N. meningitidis* as well as ATCC strains of other *Neisseriae*. We found, from digestion patterns with isoschizomers, one *N. gonorrhoeae* strain that lacked M.NgoII and two that lacked M.NgoIII. All *N. meningitidis* strains (save one) were resistant to digestion with NlaIV thus possessing an MTase like NgoV, and one was resistant to SstII, thus having an NgoIII-like MTase. None were resistant to isoschizomers of NgoI, NgoIII and NgoIV. Some other *Neisseriae* had an MTase with NlaIV (NgoV) specificity, but none had NgoI, II, III or IV specificity, except for the Branhamella-like *N. caviae-ovis* group and *N. lactamica* where these specificities were present in at least one strain of this group. Therefore, among the *Neisseriae* other than *N. caviae* only M.NgoI is *N. gonorrhoeae*-specific.

Descriptors: *DNA Modification Methylases--metabolism--ME; **Neisseria*--genetics--GE; **Neisseria gonorrhoeae*--genetics--GE; DNA Restriction Enzymes--metabolism--ME; DNA, Bacterial--metabolism--ME; Methylation; *Neisseria*--enzymology--EN; *Neisseria gonorrhoeae*--enzymology--EN

CAS Registry No.: 0 (DNA, Bacterial)

Enzyme No.: EC 2.1.1.- (DNA Modification Methylases); EC 3.1.21 (DNA Restriction Enzymes)

Record Date Created: 19900426

Record Date Completed: 19900426

06316635 89332822 PMID: 2667217
The great GATC: DNA methylation in *E. coli*.
Barras F; Marinus M G
Trends in genetics - TIG (ENGLAND) May 1989, 5 (5) p139-43, ISSN
0168-9525 Journal Code: 8507085
Document type: Journal Article; Review; Review, Tutorial
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
In *Escherichia coli* the methylation of the adenine in the sequence 5'-GATC-3' is catalysed by the dam gene product, a DNA adenine methylase. We review the proposed roles for this methylation, and the sequence it modifies, in mismatch repair, DNA-protein interaction, gene expression, the initiation of chromosome replication, chromosome segregation, chromosome structure and the occurrence of mutational hotspots. (27 Refs.)
Tags: Support, U.S. Gov't, P.H.S.
Descriptors: *DNA Modification Methylases--metabolism--ME; *DNA, Bacterial--metabolism--ME; *Escherichia coli--genetics--GE; Base Sequence; Chromosomes, Bacterial; DNA Replication; DNA, Bacterial--genetics--GE; Gene Expression Regulation; Methylation
CAS Registry No.: 0 (DNA, Bacterial)
Enzyme No.: EC 2.1.1.- (DNA Modification Methylases)
Record Date Created: 19890829
Record Date Completed: 19890829

DNA adenine methylase mutants of *Salmonella typhimurium* and a novel
dam-regulated locus.

Torreblanca J ; Casadesus J
Departamento de Genetica, Facultad de Biologia, Universidad de Sevilla,
Spain.

Genetics (UNITED STATES) Sep 1996, 144 (1) p15-26, ISSN 0016-6731
Journal Code: 0374636

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Mutants of *Salmonella typhimurium* lacking DNA adenine methylase were isolated; they include insertion and deletion alleles. The dam locus maps at 75 min between cysG and aroB, similar to the *Escherichia coli* dam gene. Dam- mutants of *S. typhimurium* resemble those of *E. coli* in the following phenotypes: (1) increased spontaneous mutations, (2) moderate SOS induction, (3) enhancement of duplication segregation, (4) inviability of dam recA and dam recB mutants, and (5) suppression of the inviability of the dam recA and dam recB combinations by mutations that eliminate mismatch repair. However, differences between *S. typhimurium* and *E. coli* dam mutants are also found: (1) *S. typhimurium* dam mutants do not show increased UV sensitivity, suggesting that methyl-directed mismatch repair does not participate in the repair of UV-induced DNA damage in *Salmonella*. (2) *S. typhimurium* dam recJ mutants are viable, suggesting that the *Salmonella* RecJ function does not participate in the repair of DNA strand breaks formed in the absence of Dam methylation. We also describe a genetic screen for detecting novel genes regulated by Dam methylation and a locus repressed by Dam methylation in the *S. typhimurium* virulence (or "cryptic") plasmid.

Tags: Support, Non-U.S. Gov't

Descriptors: **Salmonella typhimurium*--enzymology--EN; *Site-Specific DNA-Methyltransferase (Adenine-Specific)--genetics--GE; Chromosome Mapping; Cloning, Molecular; DNA Methylation; DNA Transposable Elements; Gene Deletion; Genetic Complementation Test; Mutagenesis, Insertional; *Salmonella typhimurium*--genetics--GE; *Salmonella typhimurium*--radiation effects--RE; Site-Specific DNA-Methyltransferase (Adenine-Specific)--metabolism--ME; Ultraviolet Rays

CAS Registry No.: 0 (DNA Transposable Elements)

Enzyme No.: EC 2.1.1.- (Dam methyltransferase); EC 2.1.1.72
(Site-Specific DNA-Methyltransferase (Adenine-Specific))

Record Date Created: 19970128

?logoff hold

File 155: MEDLINE(R) 1966-2003/Aug WS

(c) format only 2003 The Dialog Corp.

*File 155: Medline has been reloaded and accession numbers have changed. Please see HELP NEWS 155.

Set Items Description

Cost is in DialUnits

?ds

Set Items Description

S1 341 GATC

S2 182 S1 AND (MUTANT? OR MUTATION? OR MUTAGEN? OR ALTER? OR MODIFICATION? OR HETEROLOGO?)

S3 45 S2/1999:2003

S4 137 S2 NOT S3

S5 19 S4 AND (FOREIGN? OR HETEROLOG? OR NONNATIVE? OR FUSION? OR ANTIBIOT? OR MARKER?)

?e adenine methylase

Ref Items RT Index-term

E1 2727 ADENINE DINUCLEOTIDE //FLAVIN (FLAVIN-ADENINE DINUCLEOTIDE)

E2 4 ADENINE GLYCOSYLASE

E3 0 *ADENINE METHYLASE

E4 0 1 ADENINE NUCLEOTIDE TRANSLOCASE

E5 11 5 ADENINE NUCLEOTIDE TRANSLOCATOR 1

E6 1 ADENINE NUCLEOTIDE TRANSLOCATOR 1 --ANTAGONIST

E7 3 ADENINE NUCLEOTIDE TRANSLOCATOR 1 --BIOSYNTHES

E8 10 ADENINE NUCLEOTIDE TRANSLOCATOR 1 --GENETICS -

E9 5 ADENINE NUCLEOTIDE TRANSLOCATOR 1 --METABOLISM

E10 1 ADENINE NUCLEOTIDE TRANSLOCATOR 1 --PHYSIOLOGY

E11 1 6 ADENINE NUCLEOTIDE TRANSLOCATOR 2

E12 1 ADENINE NUCLEOTIDE TRANSLOCATOR 2 --BIOSYNTHES

Enter P or PAGE for more

?e adenine methyltransferase

Ref Items RT Index-term

E1 2727 ADENINE DINUCLEOTIDE //FLAVIN (FLAVIN-ADENINE DINUCLEOTIDE)

E2 4 ADENINE GLYCOSYLASE

E3 0 *ADENINE MethylTRANSFERASE

E4 0 1 ADENINE NUCLEOTIDE TRANSLOCASE

E5 11 5 ADENINE NUCLEOTIDE TRANSLOCATOR 1

E6 1 ADENINE NUCLEOTIDE TRANSLOCATOR 1 --ANTAGONIST

E7 3 ADENINE NUCLEOTIDE TRANSLOCATOR 1 --BIOSYNTHES

E8 10 ADENINE NUCLEOTIDE TRANSLOCATOR 1 --GENETICS -

E9 5 ADENINE NUCLEOTIDE TRANSLOCATOR 1 --METABOLISM

E10 1 ADENINE NUCLEOTIDE TRANSLOCATOR 1 --PHYSIOLOGY

E11 1 6 ADENINE NUCLEOTIDE TRANSLOCATOR 2

E12 1 ADENINE NUCLEOTIDE TRANSLOCATOR 2 --BIOSYNTHES

Enter P or PAGE for more

?e deoxyadenine methylase

Ref Items RT Index-term

E1 1 DEOXYADA

E2 722 DEOXYADENINE

E3 0 *DEOXYADENINE METHYLASE

E4 702 5 DEOXYADENINE NUCLEOTIDES

E5 2 DEOXYADENINE NUCLEOTIDES --ADMINISTRATION AND

E6 35 DEOXYADENINE NUCLEOTIDES --ANALYSIS --AN

E7 2 DEOXYADENINE NUCLEOTIDES --ANTAGONISTS AND INH

E8 8 DEOXYADENINE NUCLEOTIDES --BIOSYNTHESIS --BI

E9 30 DEOXYADENINE NUCLEOTIDES --BLOOD --BL

E10 28 DEOXYADENINE NUCLEOTIDES --CHEMICAL SYNTHESIS

E11 72 DEOXYADENINE NUCLEOTIDES --CHEMISTRY --CH

E12 1 DEOXYADENINE NUCLEOTIDES --CLASSIFICATION --CL

Enter P or PAGE for more

?e methylase

Ref	Items	Index-term
E1	2	METHYLASCORBIC
E2	9	METHYLASCORBIGEN
E3	1866	*METHYLASE
E4	854	METHYLASES
E5	466	METHYLASES //DNA MODIFICATION (DNA MODIFICATION METHYLASES)
E6	3	METHYLASIMILOBINE
E7	1	METHYLASPARAGINAMIDE
E8	10	METHYLASPARAGINE
E9	1	METHYLASPARAGINES
E10	2	METHYLASPARATE
E11	1	METHYLASPARIC
E12	21	METHYLASPARTASE

Enter P or PAGE for more

?s e5

S6 466 'METHYLASES //DNA MODIFICATION' (DNA MODIFICATION
METHYLASES)

?s s6 and adenine?

466 S6
40430 ADENINE?

S7 43 S6 AND ADENINE?

?ds

Set Items Description

S1	341	GATC
S2	182	S1 AND (MUTANT? OR MUTATION? OR MUTAGEN? OR ALTER? OR MODIFICATION? OR HETEROLOGO?)
S3	45	S2/1999:2003
S4	137	S2 NOT S3
S5	19	S4 AND (FOREIGN? OR HETEROLOG? OR NONNATIVE? OR FUSION? OR ANTIBIOT? OR MARKER?)
S6	466	'METHYLASES //DNA MODIFICATION' (DNA MODIFICATION METHYLASES)
S7	43	S6 AND ADENINE?

?s s7 not s5

43 S7
19 S5

S8 43 S7 NOT S5

?s s8/1999:2003

43 S8

2307929 PY=1999 : PY=2003

S9 13 S8/1999:2003

?s s8 not s9

43 S8
13 S9

S10 30 S8 NOT S9

06237073 89252867 PMID: 3074010

The DNA and S-adenosylmethionine-binding regions of EcoDam and related methyltransferases.

Guschlbauer W
Departement de Biologie, Centre d'Etudes Nucleaires de Saclay,
Gif-sur-Yvette, France.

Gene (NETHERLANDS) Dec 25 1988, 74 (1) p211-4, ISSN 0378-1119
Journal Code: 7706761

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Previous comparison of the amino acid sequences of the GATC-methylating Escherichia coli Dam methyltransferase (MTase) with those of other adenine MTases (M.EcoRV, M.DpnII and T4Dam) localized four conserved regions. Regions III and IV have similarities with many other MTases. The sequence DPPY (or NPPY) is always present in region IV. It was suggested to be the AdoMet binding site. Publication of the nucleotide and amino acid sequences of M.CviBIII, M.DpnA and MutH give further credence to this assignment: M.DpnA, which also methylates GATC, has strong similarities with regions III and IV; M.CviBIII, a cytosine methylase, has a characteristic NPPY sequence in region IV, and only limited resemblance in region III; MutH, the GATC-specific endonuclease in DNA mismatch repair, has significant similarities uniquely in region III. The presently available evidence suggests that region III is the GAT(C) binding site and region IV is the AdoMet binding site. This hypothesis is strengthened by recent genetic findings.

Tags: Comparative Study; Support, Non-U.S. Gov't

Descriptors: *Bacterial Proteins--metabolism--ME; *DNA Modification Methylases--metabolism--ME; *DNA, Bacterial--metabolism--ME; *Escherichia coli--enzymology--EN; *Methyltransferases--metabolism--ME; *S-Adenosylmethionine--metabolism--ME; Amino Acid Sequence; Bacterial Proteins--genetics--GE; Binding Sites; DNA Modification Methylases--genetics--GE; DNA Repair; Endodeoxyribonucleases--genetics--GE; Methyltransferases--genetics--GE; Molecular Sequence Data; Protein Binding; Protein Conformation; Sequence Homology, Nucleic Acid

CAS Registry No.: 0 (Bacterial Proteins); 0 (DNA, Bacterial);
29908-03-0 (S-Adenosylmethionine)

Enzyme No.: EC 2.1.1. (Methyltransferases); EC 2.1.1.- (DNA Modification Methylases); EC 2.1.1.- (Dam methyltransferase); EC 3.1.- (Endodeoxyribonucleases); EC 3.1.21.- (MutH gene product)

Record Date Created: 19890626

10502670 96313243 PMID: 8759008

Cloning and analysis of the genes encoding the type IIS restriction-modification system HphI from *Haemophilus parahaemolyticus*.

Lubys A; Lubiene J; Kulakauskas S; Stankevicius K; Timinskas A; Janulaitis A

Institute of Biotechnology, Vilnius, Lithuania

Nucleic acids research (ENGLAND) JUL 15 1996; 24 (14) p2760-6,
ISSN 0305-1048 Journal Code: 0411011

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The genomic region encoding the type IIS restriction-modification (R-M) system HphI (enzymes recognizing the asymmetric sequence 5'-GGTGA-3'/5'-TCACC-3') from *Haemophilus parahaemolyticus* were cloned into *Escherichia coli* and sequenced. Sequence analysis of the R-M HphI system revealed three adjacent genes aligned in the same orientation: a cytosine 5' methyltransferase (gene hphIMC), an adenine N6 methyltransferase (hphIMA) and the HphI restriction endonuclease (gene hphIR). Either methyltransferase is capable of protecting plasmid DNA in vivo against the action of the cognate restriction endonuclease. hphIMA methylation renders plasmid DNA resistant to R.HindIII at overlapping sites, suggesting that the adenine methyltransferase modifies the 3'-terminal A residue on the GGTGA strand. Strong homology was found between the N-terminal part of the m6A methyltransferase and an unidentified reading frame interrupted by an incomplete gaIE gene of *Neisseria meningitidis*. The HphI R-M genes are flanked by a copy of a 56 bp direct nucleotide repeat on each side. Similar sequences have also been identified in the non-coding regions of *H.influenzae* Rd DNA. Possible involvement of the repeat sequences in the mobility of the HphI R-M system is discussed.

Descriptors: *DNA Modification Methylases--genetics--GE; *Deoxyribonucleases, Type II Site-Specific--genetics--GE; *Haemophilus--enzymology--EN; Amino Acid Sequence; Base Sequence; Cloning, Molecular; DNA Modification Methylases--metabolism--ME; DNA, Bacterial; Deoxyribonucleases, Type II Site-Specific--metabolism--ME; Escherichia coli; Genetic Vectors; Haemophilus--genetics--GE; Molecular Sequence Data; Substrate Specificity

Molecular Sequence Databank No.: GENBANK/X85374

CAS Registry No.: 0 (DNA, Bacterial); 0 (Genetic Vectors)

Enzyme No.: EC 2.1.1.- (DNA Modification Methylases); EC 3.1.21.- (endodeoxyribonuclease HphI); EC 3.1.21.4 (Deoxyribonucleases, Type II Site-Specific)

Record Date Created: 19960917

Record Date Completed: 19960917

10469038 96276208 PMID: 8693028

Electrotransformation of highly DNA-restrictive corynebacteria with synthetic DNA.

Ankri S; Reyes O; Leblon G

Institut de Genetique et Microbiologie, Universite de Paris-Sud, Orsay, France.

Plasmid (UNITED STATES) Jan 1996, 35 (1) p62-6, ISSN 0147-619X

Journal Code: 7802221

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Highly DNA-restrictive Corynebacteria can be transformed with DNA made in vitro by PCR amplification of a sequence that contains the replication origin of pBL1, a plasmid common to many Corynebacteria. In all strains examined, the transformation efficiencies of PCR-synthetized DNA equal or improve the performances of heterologous DNA extracted from wild-type and dam(-)-dcm-strains of Escherichia coli. The transformation efficiencies obtained with PCR-made DNA may be high enough to permit its general application to experiments of gene integration.

Tags: Comparative Study; Support, Non-U.S. Gov't

Descriptors: *Corynebacterium--genetics--GE; *DNA Restriction Enzymes --metabolism--ME; *DNA, Bacterial--genetics--GE; *DNA, Recombinant --genetics--GE; *Plasmids--genetics--GE; *Transformation, Bacterial; Corynebacterium--enzymology--EN; DNA Modification Methylases--genetics--GE; DNA Modification Methylases--metabolism--ME; Electroporation; Escherichia coli--genetics--GE; Methylation; Polymerase Chain Reaction; Site-Specific DNA-Methyltransferase (Adenine -Specific)--genetics--GE; Site-Specific DNA-Methyltransferase (Adenine -Specific)--metabolism--ME

CAS Registry No.: 0 (DNA, Bacterial); 0 (DNA, Recombinant); 0 (Plasmids)

Enzyme No.: EC 2.1.1.- (DNA Modification Methylases); EC 2.1.1.- (Dam methyltransferase); EC 2.1.1.72 (Site-Specific DNA-Methyltransferase (Adenine -Specific)); EC 3.1.21 (DNA Restriction Enzymes)

Record Date Created: 19960829

Record Date Completed: 19960829

11240998 98118462 PMID: 9454710
Chlorella virus NY-2A encodes at least 12 DNA
endonuclease/methyltransferase genes.

Zhang Y; Nelson M; Nietfeldt J; Xia Y; Burbank D; Ropp S; Van Etten J L
Department of Plant Pathology, University of Nebraska, Lincoln
68583-0722, USA.

Virology (UNITED STATES) Jan 20 1998, 240 (2) p366-75, ISSN
0042-6822 Journal Code: 0110674

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Document type: Journal Article

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The 380-kb chlorella virus NY-2A genome is highly methylated; 45% of the cytosines are 5-methylcytosine (5mC) and 37% of the adenines are N6-methyladenine (6mA). Based on the sensitivity/resistance of NY-2A DNA to 80 methylation-sensitive DNA restriction endonucleases, the virus is predicted to encode at least 10 DNA methyltransferases: 7 6mA-specific methyltransferases, M.CviQI (GTmAC), M.CviQII (RmAR), M.CviQIII (TCGmA), M.CviQIV (GmATC), M.CviQV (TGCmA), M.CviQVI (GmANTC), and M.CviQVII (CmATG); and 3 5mC-specific methyltransferases, M.CviQVIII [RGmC(T/C/G)], M.CviQIX (mCC), and M.CviQX (mCGR). Five of the 6mA methyltransferase genes, M.CviQI, M.CviQIII, M.CviQV, M.CviQVI, and M.CviQVII, were cloned and sequenced. In addition, 2 site-specific endonuclease activities, R.CviQI (G/TAC) and NY2A-nickase (R/AG), were detected in cell-free extracts from NY-2A virus-infected chlorella. Therefore, the NY-2A genome contains at least 12 DNA methyltransferase and endonuclease genes which, altogether, compose about 3-4% of the virus genome.

Tags: Support, U.S. Gov't, P.H.S.

Descriptors: *Chlorella--virology--VI; *DNA Modification Methylases--genetics--GE; *Deoxyribonuclease I--genetics--GE; *Phycodnaviridae--genetics--GE; Amino Acid Sequence; DNA Methylation; DNA Modification Methylases--isolation and purification--IP; Deoxyribonuclease I--isolation and purification--IP; Genes, Viral--genetics--GE; Molecular Sequence Data; Phycodnaviridae--enzymology--EN; Sequence Alignment; Sequence Homology, Amino Acid

Molecular Sequence Databank No.: GENBANK/AF021248; GENBANK/AF021249; GENBANK/AF021250; GENBANK/AF021251; GENBANK/AF021252

Enzyme No.: EC 2.1.1.- (DNA Modification Methylases); EC 3.1.21.1 (Deoxyribonuclease I)

Record Date Created: 19980220

Record Date Completed: 19980220

these leaky mutants retain endonucleolytic activity; strong binding, without cleavage, to all EcoRI sites in the *E. coli* genome is likely to be toxic. It is likely that leaky mutants can be expressed in cells that also express the EcoRI methylase activity so that the proteins can be characterized. Leaky mutants that lack nuclease activity or EcoRI-delN29 could be used as an initial DBP for DNA targets related to the EcoRI sequence. The non-binding mutants, AT139, GS140, and RQ203, could also be used as initial DBPs; alterations or extension of the protein in such a way that additional base pairs are contacted will supply the free-energy lost through these mutations. Yanofsky et al. state that most null mutants of EcoRI accessible through hydroxylamine have probably been identified. Other mutants are likely to be revealed by other mutagens. Null mutants are, however, selected not only for lack of nuclease activity, but also for non-binding, and therefore are not so useful as leaky mutants.

Detailed Description Text (383):

First, each enzyme that has a unique possible site is picked; if two of these overlap, then the better enzyme is picked. An enzyme is better if it: a) generates cohesive ends, b) has unambiguous recognition, c) has higher specific activity, or d) (for work in *E. coli*) is not sensitive to dam or dcm methylation. Next, those sites close to other sites already picked are eliminated because many sites very close together are not useful. Finally, sites are chosen to minimize the size of the longest piece between restriction sites.

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	KMPC	Draw Desc
Image											

92. Document ID: US 5194387 A

L14: Entry 92 of 106

File: USPT

Mar 16, 1993

DOCUMENT-IDENTIFIER: US 5194387 A

TITLE: Process for the incorporation of DNA molecules into microorganisms with methyl-specific restriction systems

Brief Summary Text (2):

The introduction of foreign DNA, including plasmids, phages, and chromosomal DNA fragments, into microorganisms is a well established procedure. However, certain microorganisms cleave and inactivate foreign DNA through restriction systems making it difficult or impossible to introduce foreign DNA into these microorganisms. Restriction-modification systems are widespread in microorganisms. Most restriction-modification systems are composed of a methylase and an endonuclease. The modification enzyme (methylase) modifies the host DNA at a specific sequence composed of 4 or more bases, and the restriction endonuclease cleaves unmodified, foreign DNA at or near the specific sequence (for a review see Kessler et al. Gene 47 pg. 1-153 (1986)). Over 600 restriction endonucleases and 98 methylases are known. Three methyl-specific restriction systems have been described. In strains with methyl-specific restriction systems, foreign, methyl modified DNA is restricted and the host "modification" is the lack of modified DNA. *Diplococcus pneumoniae* restricts DNA containing N.sup.6 -methyladenine at the sequence GATC. Two other strains restrict DNA containing 5-methylcytosine, but these strains show little or no sequence specificity.

Brief Summary Text (15):

The restriction shown by *S. avermitilis* is not limited to DNA isolated from *E. coli*, but also restricts DNA from a modification proficient *Streptomyces*. This was determined by isolating DNA from *S. griseus*. *S. griseus* is a known host for pVE1 derivatives, although it restricts the entry of DNA from *S. avermitilis* and *S. lividans* (see Table 3). When *S. griseus* was transformed with pVE28, only a derivative, which was 0.4 kb smaller than pVE28, was isolated from the transformants. This deletion derivative was designated pVE614. When pVE614 is isolated from *S. griseus* it is resistant to cleavage by SstI. However, when pVE614 is isolated from *S. lividans*, it is cleaved by SstI at a single site, the parental plasmid pVE28 contains two SstI sites, but one site is within the 0.4 kb region deleted to form pVE614. Evidently, *S. griseus* contains a restriction-modification system which modifies the DNA that overlaps the SstI site. When pVE614 was isolated from *S. griseus* it could be used to transform *S. lividans*, but not *S. avermitilis*. This was due to restriction, rather than problems with the maintenance or replication of pVE614, because pVE614 DNA isolated from *S. lividans* will efficiently transform *S. avermitilis* (see Table 3). Thus, *S. avermitilis* contains a restriction system which restricts the entry of DNA from *E. coli* RR1, known to contain the dam and dcm modification systems, and from *S. griseus*, shown here to modify DNA at or near a SstI site in pVE614.

Detailed Description Text (2):

Since *S. avermitilis* does not restrict DNA isolated from *S. lividans*, *S. lividans* must process DNA in one of two ways so that DNA is not cleaved by *S. avermitilis* restriction enzymes. *S. lividans*, a species unrelated to *S. avermitilis*, could coincidentally modify the sites in DNA recognized by a *S. avermitilis* restriction-modification system. Alternatively, *S. avermitilis* might contain a methyl-specific restriction system and *S. lividans* might not methylate DNA. This latter possibility was tested by transforming *S. avermitilis* protoplasts with pVE28, a 4.9 kb, high copy number *Streptomyces* plasmid that was modified in vitro with various methylases. Table 4 shows that *S. avermitilis* strongly restricted DNA that was modified with Alul, dam, HhaI, HphI, and TagI methylases, the efficiency of transformation (eot) was reduced between 10⁻³ and 10⁻⁴. The 4 or 5 bp recognition sites for these methylases occur frequently in the DNA tested. pVE28 and other pVE1 derivatives with only 1, 2, or 3 sites for in vitro methylation were only weakly restricted since their efficiency of transformation was reduced only about 10 fold (see Table 4). This indicates that the probability of a DNA molecule being restricted by *S. avermitilis* is proportional to the number of methylated bases it contains. There appears to be no sequence specificity to the methyl-specific restriction observed in *S. avermitilis*, since all 8 methylases tested reduced the eot of the modified plasmids. *S. avermitilis* restricts both 5'-methylcytosine and N⁶-methyladenine modified DNA.

Detailed Description Text (4):

E. coli RR1, the host for the shuttle vectors in Table 2, contains two DNA methylases. The dcm product modifies the sequence GG(AT)CC to produce 5-methylcytosine and the dam product modifies the sequence GATC yielding N⁶-methyladenine. As shown above, *S. avermitilis* restricts modified DNA, this could explain why *S. avermitilis* can not be transformed by shuttle vectors isolated from *E. coli* RR1. To test if the dcm and dam modifications cause *S. avermitilis* to restrict shuttle vectors isolated from *E. coli*, shuttle vectors were isolated from a methylase deficient *E. coli* GM272 (dcm,dam,hsd). As Table 5 shows, DNA from GM272 could be transformed directly into *S. avermitilis*. However, the plasmids isolated from GM272 still showed a reduced efficiency of transformation compared to plasmids isolated from *Streptomyces*. The residual restriction of DNA isolated from GM272 may be because the dam and dcm mutations in GM272 do not completely eliminate all DNA methylation. This was tested by comparing the restriction enzyme digestion pattern of shuttle vector DNA isolated from GM272 and *Streptomyces* which had been cleaved with methylation sensitive enzymes. When pVE3 and pVE328 DNAs isolated from GM272 were cleaved with MboI and EcoRII, faint bands resulting from only partial cleavage were visible. In contrast, the shuttle vectors DNAs isolated from *Streptomyces* were cleaved to completion. Thus, it is likely the restriction seen when DNA from GM272 is introduced into *S. avermitilis* is the result of the residual methylase activity in GM272.

recombination in lacZ (Konrad, E. B. 1977. J. Bacteriol. 130:167-172). No demonstration of RecA-independent microhomologous recombination in vitro has been reported.

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	KM/C	Drawn Desc
<input type="checkbox"/> Image											

89. Document ID: US 5202256 A

L14: Entry 89 of 106

File: USPT

Apr 13, 1993

DOCUMENT-IDENTIFIER: US 5202256 A

TITLE: Bioadhesive precursor protein expression vectors

Detailed Description Text (137):

An in-frame gene fusion between the trpB portion of pGX2346, and the bioadhesive precursor protein cDNA of pGX2368 is constructed in the following manner: A BclI endonuclease recognition site was first placed at the translation stop codon of pGX2368 by changing two bases as indicated in FIG. 1 using oligonucleotide-directed mutagenesis (Zoller, M. J. and M. Smith, Methods Enzymol., 100:457-500, 1983) to create plasmid pGX2380. Both plasmids pGX2380 and pGX2346 are grown for DNA preparation in an *E. coli* host that contains the dam mutation (defective in DNA adenine methylase) so that they could be digested with BclI. The non-methylated pGX2346 DNA is cut with NotI and the pGX2380 DNA is cut with XbaI. Then both DNAs are treated with *E. coli* DNA polymerase (Klenow fragment) to fill in the 5' single-stranded DNA overhangs. The DNAs are then ligated at high DNA concentration (approximately 2 ug of each DNA in 20 ul) with T4 ligase. The ligation product is cut with BclI then ligated again at low DNA concentration (approximately 1 ug total DNA in 150 ul volume) and used to transform *E. coli* GX3015. A transformant with the desired construction (see FIG. 6) is designated pGX2383. GX3015 cells with plasmid pGX2383 produce a bioadhesive precursor protein of approximately 24,000 M.W. upon induction of the hybrid lambda promoter by a shift of growth temperature from 32.degree. to 37.degree. C.

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	KM/C	Drawn Desc
<input type="checkbox"/> Image											

90. Document ID: US 5202236 A

L14: Entry 90 of 106

File: USPT

Apr 13, 1993

DOCUMENT-IDENTIFIER: US 5202236 A

TITLE: Method of producing bioadhesive protein

Detailed Description Text (138):

An in-frame gene fusion between the *trpB* portion of pGX2346, and the bioadhesive precursor protein cDNA of pGX2368 is constructed in the following manner: A *BclI* endonuclease recognition site was first placed at the translation stop codon of pGX2368 by changing two bases as indicated in FIG. 1 using oligonucleotide-directed mutagenesis (Zoller, M. J. and M. Smith, Methods Enzymol., 100:457-500, 1983) to create plasmid pGX2380. Both plasmids pGX2380 and pGX2346 are grown for DNA preparation in an *E. coli* host that contains the dam mutation (defective in DNA adenine methylase) so that they could be digested with *BclI*. The non-methylated pGX2346 DNA is cut with *NotI* and the pGX2380 DNA is cut with *XbaI*. Then both DNAs are treated with *E. coli* DNA polymerase (Klenow fragment) to fill in the 5' single-stranded DNA overhangs. The DNAs are then ligated at high DNA concentration (approximately 2 ug of each DNA in 20 ul) with T4 ligase. The ligation product is cut with *BclI* then ligated again at low DNA concentration (approximately 1 ug total DNA in 150 ul volume) and used to transform *E. coli* GX3015. A transformant with the desired construction (see FIG. 6) is designated pGX2383. GX3015 cells with plasmid pGX2383 produce a bioadhesive precursor protein of approximately 24,000 M.W. upon induction of the hybrid lambda promoter by a shift of growth temperature from 32.degree. to 37.degree. C.

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	KIMC	Drawn Desc
Image											

 91. Document ID: US 5198346 A

L14: Entry 91 of 106

File: USPT

Mar 30, 1993

DOCUMENT-IDENTIFIER: US 5198346 A

TITLE: Generation and selection of novel DNA-binding proteins and polypeptides

Detailed Description Text (37):

Most strains of *E. coli* contain the dam and dcm DNA-methylating systems. The Dam methylase transfers a methyl from S-adenosylmethionine (SAM) to the N._{sub}6 of adenine residues in the subsequence GATC. The Dcm methylase transfers a methyl from SAM to the internal cytosine in the sequences CCAGG and CCTGG. If a DBP is desired that will bind to unmethylated DNA, and if the target sequence contains either the Dam or Dcm recognition sequence, then a Dam.sup.- or Dcm.sup.- strain should be used.

Detailed Description Text (215):

Yanofsky et al. (YAN087) report a number of mutants of EcoRI obtained by mutagenesis of a plasmid-borne gene with hydroxylamine and expression in cells lacking the EcoRI methylase activity. The initial gene comprises the lacUV5 promoter and a coding region that codes on expression for the EcoRI endonuclease. Three of the mutants could be expressed at high levels and were shown to be dimeric, viz. AT139, GS140, and RQ203; these mutations prevent protein-DNA binding. Other mutants (viz. LF46, RQ56, GE129, AT142, GE210, and SL259) of the ecoRI gene were obtained that were "leaky", i.e. they were lethal if induced with 1.0 mM IPTG. (This level of IPTG induces lacUV5 to the maximum extent.) The authors do not report whether

DOCUMENT-IDENTIFIER: US 5849305 A
TITLE: Construction of *Pasteurella haemolytica* vaccines

Abstract Text (1):

Methylation of DNA can be a critical step in the introduction of DNA into *P. haemolytica*. A methyltransferase has been isolated and molecularly cloned for this purpose. Use of the methyltransferase has allowed construction of defined, attenuated mutants for use as vaccines to protect cattle.

Detailed Description Text (39):

After digestion with PhaI and transformation of AP1-200-9 strain of *E. coli*, fifteen cosmid clones of *P. haemolytica* genomic DNA were tested for endonuclease activity. The nine clones which were endonuclease-positive were tested for PhaI methyltransferase activity. All nine expressed methyltransferase activity in addition to endonuclease activity, as evidenced by resistance to digestion by PhaI of genomic DNA recovered from transformed *E. coli*. The selective recovery of clones containing functional methyltransferase was due to previous digestion of the cosmid library with PhaI prior to transformation of *E. coli*. Recovery of clones containing both PhaI endonuclease and methyltransferase activity is not surprising since restriction and modification enzymes have previously been shown to be closely linked (the proximity of such genes has obvious implications to gene inheritance and the survival of the organism). The AP1-200-9 strain of *E. coli* (used to screen the cosmid library in this experiment) was designed by Piekarowicz et al., to give color selection for DNA-modifying enzymes (genes). The mrr and mcr systems, with a temperature-sensitive phenotype, induce inducible locus of the SOS response allows for color selection. All the transformants were blue after incubation at the permissive temperature for the mcr/mrr systems. Recovery of clones containing both PhaI endonuclease and methyltransferase activity is not surprising since restriction and modification enzymes have previously been shown to be closely linked (the proximity of such genes has obvious implications to gene inheritance and to the survival of the organism). (Wilson et al., Annu. Rev. Genet. 25:585-627 (1991).)

Detailed Description Text (50):

The possibility that a system similar to *E. coli* mcr, mrr, is active in *P. haemolytica* was investigated by passage of pPhDELTA.roACm.sup.R pD80 through *E. coli* strain GM2163 previously transformed with the recombinant cosmid containing PhaI methyltransferase (Raleigh et al., Proc. Natl. Acad. Sci. 83:9070-9074 (1986)). Since strain GM2163 is dam-, the resultant DNA would only be modified at PhaI sites (Marinus et al., Mol. Gen. Genet. 192:288-289 (1983)). Efficiency of transformation with this DNA, however, was not substantially different than that using DNA obtained from PhaI Mtase which is dam-methylated (Table 1). It is possible a second restriction system, not readily detectable in cell extracts, is active in *P. haemolytica* A1. Genes have been described in *Neisseria gonorrhoea* MS11 which encode for restriction enzymes which are expressed at levels too low to detect biochemically (Stein et al., J. Bact. 74:4899-4906 (1992)).

Detailed Description Text (62):

Construction of a *P. haemolytica* aroA mutant. The deletion plasmid, pPh.DELTA.aroACm.sup.R (Table 2), was constructed from pPharoA2 as described above and amplified in E. coli containing a cosmid clone carrying the PhaI methyltransferase gene on a 20-kb *P. haemolytica* DNA fragment. Although resistant to PhaI endonuclease digestion, introduction of pPh.DELTA.aroACm.sup.R into *P. haemolytica* strain NADC-D60 by electroporation failed to generate Cm resistant colonies. The inability to transform *P. haemolytica* with pPh.DELTA.aroACm.sup.R suggested that plasmids containing a CoIE1 origin do not replicate in this bacterium.

Detailed Description Text (64):

WEST Search History

DATE: Thursday, August 21, 2003

<u>Set</u>	<u>Name</u>	<u>Query</u>	<u>Hit</u>	<u>Set</u>
			<u>Count</u>	<u>Name</u>
	side by side			result set
		DB=USPT; PLUR=YES; OP=AND		
L1		dam.clm.	3181	L1
L2		(\$methylase or methyltransferase\$ or methyl-transferase\$).clm.	241	L2
L3		L2 or dna.clm.	17060	L3
L4		L3 and l1	18	L4
L5		dam same (bacter\$ or microorgan\$ or salmonel\$ or shigel\$ or coli)	446	L5
L6		dam same (prokaryot\$ or procaryot\$)	13	L6
L7		L5 not l6 not l4	425	L7
L8		(\$methylase or methyltransferase\$ or methyl-transferase\$)	2250	L8
L9		L8 and l7	153	L9
L10		L9 and (heterologous or foreign or nonnative or recombinant or artificial or fusion)	152	L10
L11		L9 and (heterologous or foreign or nonnative or fusion)	121	L11
L12		L9 and (heterologous or foreign or nonnative or fusion)	121	L12
L13		(\$methylase or methyltransferase\$ or methyl-transferase\$ or dam) near50 (mutant or mutation or mutagenesis or alter\$ or mutants or mutations or insertion or deletion or modification or modified or truncated or truncation)	1690	L13

L14 L13 and 15

106 L14

END OF SEARCH HISTORY